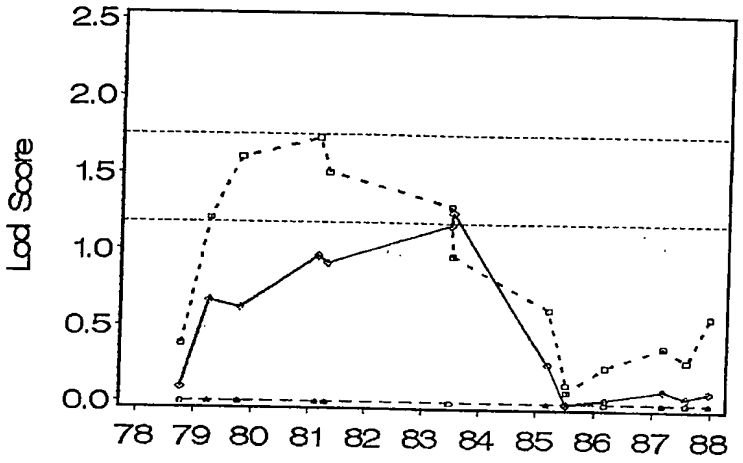
A


Lod Score
2.5
2.0
1.5
1.0
0.5
0.0
78 79 80 81 82 83 84 85 86 87 88

B

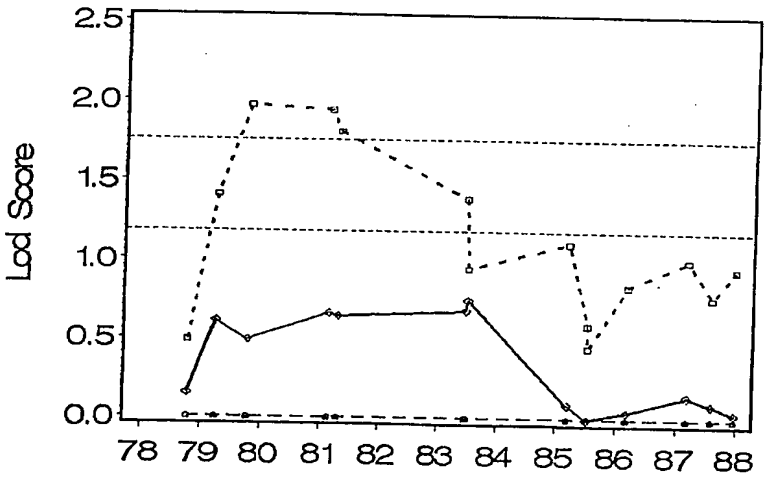

Lod Score
2.5
2.0
1.5
1.0
0.5
0.0
78 79 80 81 82 83 84 85 86 87 88

Fig. 1

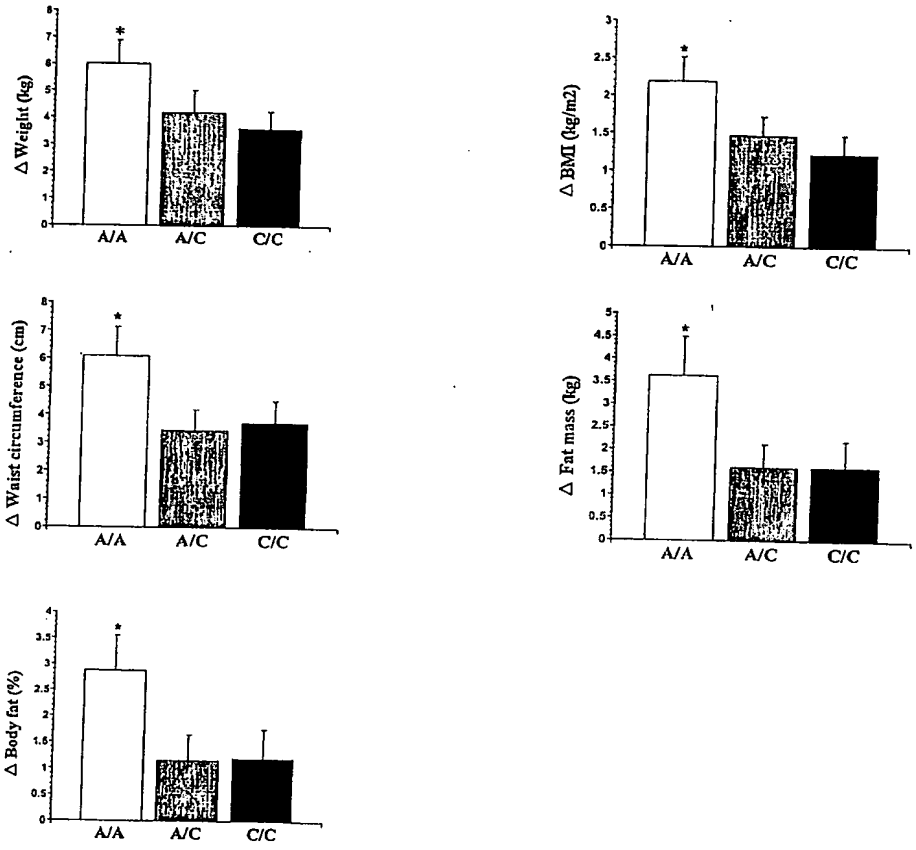

Δ Weight (kg)
Δ BMI (kg/m2)
Δ Waist circumference (cm)
Δ Fat mass (kg)
Δ Body fat (%)
A/A
A/C
C/C
*

Fig. 2

Homo sapiens
MARRAGGARMFGSLLLFALLAAGVAPLSWDLPEPRSRASKIRVHSRGNLWATGHFMGKKS 60

Mus musculus
MTRQAGSSWLLRGLLLFALFASGVAPFNWDLPEPRSRASKIRVHPRGNLWATGHFMGKKS 60

Homo sapiens
LEPSSPSPLGTAPHTSLRDQRLQLSHDLLGILLLKKALGVSLSRPAPQIQYRRLLVQILQK 121

Mus musculus
LEPPSLSLVGTAPPNTPRDQRLQLSHDLLRILLRKKALGMNFSGPAPPIQYRRLLEPLLQK 121

Fig. 3

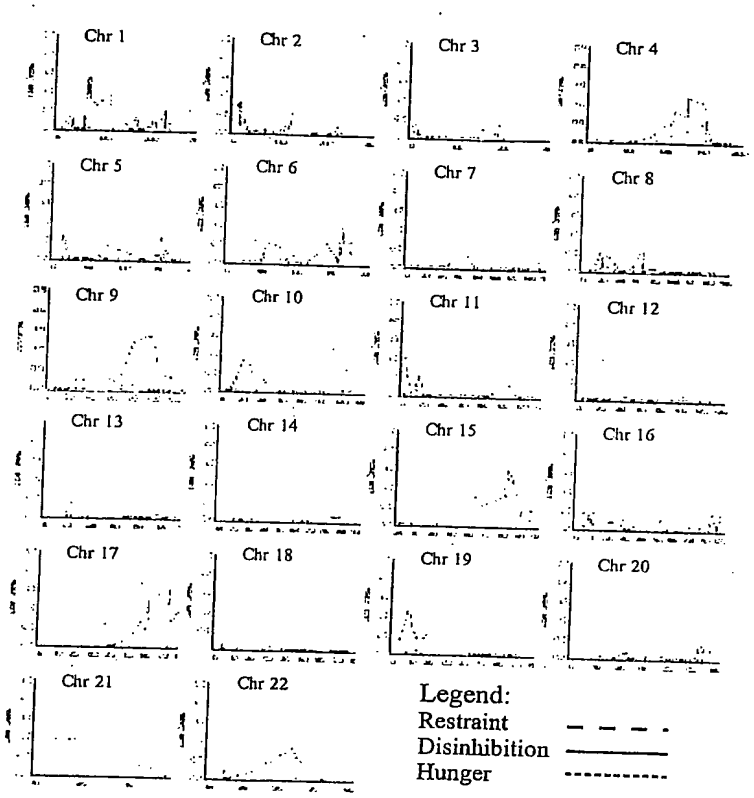

Chr 1
Chr 2
Chr 3
Chr 4
Chr 5
Chr 6
Chr 7
Chr 8
Chr 9
Chr 10
Chr 11
Chr 12
Chr 13
Chr 14
Chr 15
Chr 16
Chr 17
Chr 18
Chr 19
Chr 20
Chr 21
Chr 22
Legend:
Restraint
Disinhibition
Hunger

Fig. 4

NMB_REF
CTGTTACCCGGGAGGAGAGCTCCTCGCCCGACCTCTACCCTCATGAAGAGAGGCTCAGAG 60
NMB_MUT
CTGTTACCCGGGAGGAGAGCTCTTCGCCCGACCTCTACCCTCATGAAGAGAGGCTCAGAG

NMB_REF
GGCTGAAGTGCCTATTTGGCCGAAAGCCGTGGCAGAGTGGCAAGGCAGGGCCAGGGGAAG 120
NMB_MUT
GGCTGAAGTGCCTATTTGGCCGAAAGCCGTGGCAGAGTGGCAAGGCAGGGCCAGGGGAAG

NMB_REF
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NMB_MUT
CGGCTCCGCCGCCGGGGCCGGGCCCCTGTTTGGCCGGTGCCCGGTCCTTAGCCTGAAGGT

NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
GTGTGCAGGTCTCTGGGCGGCCCAAAGGGGGTGCCCCTGCCTGGTAACCTAGCGGGAGGG

NMB_REF
TGGGGACGGCGGGGAGGGCGGCGGGCGCGGGGCACGGCTCCGCTGCTCAGGGCAGGCTCC 360
NMB_MUT
TGGGGACGGCGGGGAGGGCGGCGGGCGCGGGGCACGGCTCCGCTGCTCAGGGCAGGCTCC

NMB_REF
GCCCCCAGGGGCGCGGATTTAAAAGGATCGAAGGCAGCCCCGGAGCCCAGCGGCCGGGAA 420
NMB_MUT
GCCCCCAGGGGCGCGGATTTAAAAGGATCGAAGGCAGCCCCGGAGCCCAGCGGCCGGGAA

NMB_REF
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NMB_MUT
GCGCGCCCGAACGAAGCCGCGGCCCGGGCACAGCCATGGCCCGGCGGGCGGGGGGCGCTC

NMB_REF
GGATGTTCGGCAGCCTCCTGCTCTTCGCCCTGCTCGCTGCCGGCGTCGCCCCGCTCAGCT 540
NMB_MUT
GGATGTTCGGCAGCCTCCTGCTCTTCGCCCTGCTCGCTGCCGGCGTCGCCCCGCTCAGCT

Fig. 5

NMB_REF
GGGATCTCCCGGAGCCCCGCAGCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAACC 600
NMB_MUT
GGGATCTCCCGGAGCCCCGCAGCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAACC

NMB_REF
TCTGGGCCACCGGTAAGTCTTTGGGGACGGAGCAAGCAAGCGCCCCTCATCCAGTTCAGA 660
NMB_MUT
TCTGGGCCACCGGTAAGTCTTTGGGGACGGAGCAAGCAAGCGCCCCTCATCCAGTTCAGA

NMB_REF
CCCCATTTCCTTCTCAACCCTCTGGCCGCTCCTCAGCCACGGACACTAGTGTCGGAGCAG 720
NMB_MUT
CCCCATTTCCTTCTCAACCCTCTGGCCGCTCCTCAGCCACGGACACTAGTGTCGGAGCAG

NMB_REF
GTGGAAAACCCTGGGGCTCATCTAATTTAATAGATATGTACTTGAGACCCGGACAGGTCA 780
NMB_MUT
GTGGAAAACCCTGGGGCTCATCTAATTTAATAGATATGTACTTGAGACCCGGACAGGTCA

NMB_REF
GTGACTTGGCTAAGGTCGCGCAGCCAGTTTAAGACAGGGCTGGGCTAGATCCTAAATCCC 840
NMB_MUT
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NMB_REF
ACTGCCAGCCGGTGCCCCTTACCTTAGGCGAGACTTAACCGAATCTTCTAACCGCTGGTG 900
NMB_MUT
ACTGCCAGCCGGTGCCCCTTACCTTAGGCGAGACTTAACCGAATCTTCTAACGGCTGGTG

NMB_REF
TGTTTTTGCTGCACCTCCACTTTCCAGGCGCCTCTTCACTCTCCACTTCCTACCCTGCCC 960
NMB_MUT
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NMB_REF
TTTTTCGTCCCTTGTCCAAGCAGCCCACACAACTAGCAGAGTTTCTCCCTGGCCCTGGAC 1020
NMB_MUT
TTTTTCGTCCCTTGTCCAAGCAGCCCACACAACTAGCAGAGTTTCTCCCTGGCCCTGGAC

NMB_REF
CATCCCACCTTCCTGCCAGCTGTGCCATCCTCTCTACCTGTTCAGGAAAAGCTGAGGGAG 1080
NMB_MUT
CATCCCACCTTCCTGCCAGCTGTGCCATCCTCTCTACCTGTTCAGGAAAAGCTGAGGGAG

Fig. 5 (cont')

NMB_REF
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NMB_MUT
CAGGATTTGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAGGTGGAAGCACCAAGAG

NMB_REF
GAGGAAGGTTAAGTGTCTTCCCGCTACAAGAACGGAAACGTGGGAGAGATGAGGAACTTT 1200
NMB_MUT
GAGGAAGGTTAAGTGTCTTCCCGCTACAAGAACGGAAACGTGGGAGAGATGAGGAACTTT

NMB_REF
TCCTCTGAGGTAGGATCCTGGCTGCTTGACTTCCTTGTGCCTGGACACCTCCTTTCCAGG 1260
NMB_MUT
TCCTCTGAGGTAGGATCCTGGCTGCTTGACTTCCTTGTGCCTGGACACCTCCTTTCCAGG

NMB_REF
TCACTTCATGGGCAAGAAGAGTCTGGAGCCTTCCAGCCCATCCCCATTGGGGACAGCTCC 1320
NMB_MUT
TCACTTCATGGGCAAGAAGAGTCTGGAGCCTTCCAGCCCATCCCCATTGGGGACAGCTAC

NMB_REF
CCACACCTCCCTGAGGGACCAGCGACTGCAGCTGAGTCATGATCTGCTCGGAATCCTCCT 1380
NMB_MUT
CCACACCTCCCTGAGGGACCAGCGACTGCAGCTGAGTCATGATCTGCTCGGAATCCTCCT

NMB_REF
GCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCCGCACCCCAAATCCAGGTGAGCCG 1440
NMB_MUT
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NMB_REF
GGCCCCTGCTCCAATGTCAGGAGGGCCCAGCTGGGGCCATCCCCGGATCCTGCATGGGAG 1500
NMB_MUT
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NMB_REF
GAATTACCACCCAGTACTGTATTAGGGTGTGACTGTCTGACTAGGACATTATGGGTGTGG 1560
NMB_MUT
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NMB_REF
ACCCCAGAAAGCCAGGTTTCCAGGCTTTTCCCTCTTGAGGCAGAGCTCAAAGGAGGAACA 1620
NMB_MUT
ACCCCAGAAAGCCAGGTTTCCAGGCTTTTCCCTCTTGAGGCAGAGCTCAAAGGAGGAACA

Fig. 5 (cont')

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NMB_MUT
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NMB_REF
AGTTCCCCTGACTCATCACCCAGTCTAAAGTAACAGACTGGGATCATCAGCCTTTTGGAG 1740
NMB_MUT
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NMB_REF
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NMB_MUT
CAGGACCTTTCTCCCCCAGTCTACACAGTCTTGTCCCACCCATGCTGTTCCCTGCTGCAT

NMB_REF
TAGTCAAGTCCACCTTTGCTGTGTCCTGTGTATGCTTGTGGCCGGAATGGGACCCTGAGG 1860
NMB_MUT
TAGTCAAGTCCACCTTTGCTGTGTCCTGTGTATGCTTGTGGCCGGAATGGGACCCTGAGG

NMB_REF
CCCAGAGAGGGAAAGAGAAGTCAGCAGCCAAGACAGAGTCTGGACCTTGTTCACCTGGAC 1920
NMB_MUT
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NMB_REF
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NMB_REF
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NMB_REF
GGATGTTTGGCAGCATCCCTGGTCTCTACATACTAGATGCCAGTAGCATCTTTCCCCCCC 2100
NMB_MUT
GGATGTTTGGCAGCATCCCTGGTCTCTACATACTAGATGCCAGTAGCATCTTTCCCCCCC

NMB_REF
ATCAAGTTGTGACAACTGAAAAGACCTCCAGACATCACCAGATGTCTGCTGGGGGAGAGG 2160
NMB_MUT
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Fig. 5 (cont')

NMB_REF
GCCCCAAATCATTATTGGTTGTCAGTCACTGATCTATGGGATTCAAGACTCCAAAGCTGG 2220
NMB_MUT
GCCCCAAATCATTATTGGTTGTCAGTCACTGATCTATGGGATTCAAGACTCCAAAGCTGG

NMB_REF
AGCCAAGCTAGCCTCAAGGTATAGCCCCGCTGAGTGGCAACTCCTTCATTCCCTGCTCCT 2280
NMB_MUT
AGCCAAGCTAGCCTCAAGGTATAGCCCCGCTGAGTGGCAACTCCTTCATTCCCTGCTCCT

NMB_REF
GGTGCTGTCCTTACTGCACACCACCCTCCCTGGTCCTGCTGCTGTGTGCAGAAGGCAGTG 2340
NMB_MUT
GGTGCTGTCCTTACTGCACACCACCCTCCCTGGTCCTGCTGCTGTGTGCAGAAGGCAGTG

NMB_REF
TGATGTGGTAGAATGTGGGTTTTGACTACAACGTGCTGGGCTCATAACCTAGCTACTTAG 2400
NMB_MUT
TGATGTGGTAGAATGTGGGTTTTGACTACAACGTGCTGGGCTCATAACCTAGCTACTTAG

NMB_REF
TAGCTGTATGACCTTAGAAATGTCCCTTAACTTCTCTAAAGCCTCAATATTCTTCACCCA 2460
NMB_MUT
TAGCTGTATGACCTTAGAAATGTCCCTTAACTTCTCTAAAGCCTCAATATTCTTCACCCA

NMB_REF
TAAAATGAAGATAATAAGGCCCATCTCCCATTAAATGAGACCATTTATGTCAAATGCTCA 2520
NMB_MUT
TAAAATGAAGATAATAAGGCCCATCTCCCATTAAATGAGACCATTTATGTCAAATGCTCA

NMB_REF
GCATGGTGCCTGGCTCATAGACAGCCCTTAGTAGATGCGAGCTCTTATCAGTCTGTGAGC 2580
NMB_MUT
GCATGGTGCCTGGCTCATAGACAGCCCTTAGTAGATGCGAGCTCTTATCAGTCTGTGAGC

NMB_REF
TCCCTGGCGGCACCTGTTGTAGACTCGCCTTCATATCCCCCAGTGTGCCTAGCATATAGT 2640
NMB_MUT
TCCCTGGCGGCACCTGTTGTAGACTCGCCTTCATATCCCCCAGTGTGCCTAGCATATAGT

NMB_REF
GTGTGCATTTTGAAGGGAGAGGCATTCCCTAGAAAAGGTCCAACCCAGCCTCAACCAACA 2700
NMB_MUT
GTGTGCATTTTGAAGGGAGAGGCATTCCCTAGAAAAGGTCCAACCCAGCCTCAACCAACA

Fig. 5 (cont')

NMB_REF
TCCCTGACTTCCTGAGGCACAGAACCAGCAGCCCCTGAGGACCTCAGATGTAAGGCCTAG 2760
NMB_MUT
TCCCTGACTTCCTGAGGCACAGAACCAGCAGCCCCTGAGGACCTCAGATGTAAGGCCTAG

NMB_REF
GAGCTTGGGCTGGCTGAGTCTGAAGGGAAACAATGTCACCTCTAATGCCCTTGGTTTTGA 2820
NMB_MUT
GAGCTTGGGCTGGCTGAGTCTGAAGGGAAACAATGTCACCTCTAATGCCCTTGGTTTTGA

NMB_REF
AGCTCTGACACATGCAGACCAACTAGAGAATCTCAGAAGCAGCAGTGCCTACGTCTGGGG 2880
NMB_MUT
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NMB_MUT
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NMB_REF
AGCACCAAGCACTGTATTTGGATTTTCTTCCACGATCTTCTTTGACTGTCATGACCACCC 3000
NMB_MUT
AGCACCAGGCACTGTATTTGGATTTTCTTCCACGATCTTCTTTGACTGTCATGACCACCC

NMB_REF
TGGGTGGTTGGGGCTGTGTTCTGAGAAAACTACTGCCCCGACCCCTCCAAGGCAATTCAG 3060
NMB_MUT
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NMB_REF
GGTGCTCTGGGGCCTGCCTCAGCTGACAGCCTGCTGGTGCCCACCTCTGCAGACATCTGG 3120
NMB_MUT
GGTGCTCTGGGGCCTGCCTCAGCTGACAGCCTGCTGGTGCCCACCTCTGCAGACATCTGG

NMB_REF
CACTTAGGAATGGCAGGATGCCCCTATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTT 3180
NMB_MUT
CACTTAGGAATGGCAGGATGCCCCTATCTTTATCAGGAGCCCTTCCCTGGCTCAATTCTT

NMB_REF
CTGTATGTTTCTCTTCAGTACAGGAGGCTGCTGGTACAAATACTGCAGAAATGACACCAA 3240
NMB_MUT
CTGTATGTTTCTCTTCAGTACAGGAGGCTGCTGGTACAAATACTGCAGAAATGACACCAA

Fig. 5 (cont')

NMB_REF
TAATGGGGCAGACACAACAGCGTGGCTTAGATTGTGCCCACCCAGGGAAGGTGCTGAATG 3300
NMB_MUT
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NMB_REF
GGACCCTGTTGATGGCCCCATCTGGATGTAAATCCTGAGCTCAAATCTCTGTTACTCCAT 3360
NMB_MUT
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NMB_REF
TACTGTGATTTCTGGCTGGGTCACCAGAAATATCGCTGATGCAGACACAGATTATGTTCC 3420
NMB_MUT
TACTGTGATTTCTGGCTGGGTCACCAGAAATATCGCTGATGCAGACACAGATTATGTTCC

NMB_REF
TGCTGTATTTCCTGCTTCCCTGTTGAATTGGTGAATAAAACCTTGCTCTTTACATACAAT 3480
NMB_MUT
TGCTGTATTTCCTGCTTCCCTGTTGAATTGGTGAATAAAACCTTGCTCTTTACATAAAAT

NMB_REF
GCCTGGTCCTCTCCTTTCACCCGTCTTTTAGGGGATGGGAGGAAAAGGGGGCTGGAGGGC 3540
NMB_MUT
GCCTGGTCCTCTCCTTTCACCCGTCTTTTAGGGGATGGGAGGAAAAGGGGGCTGGAGGGC

NMB_REF
AGAGTGTTCAGTGAGATGGGGCTGGCTCAAAAAGTCCAGAATACCCCATGCCATGGCACC 3600
NMB_MUT
AGAGTGTTCAGTGAGATGGGGCTGGCTCAAAAAGTCCAGAATACCCCATGCCATGGCACC

NMB_REF
AGCCTGGCACTGACTCTGGCCTCCTACCCATTCATTCAGCAAGCAAATAACGCCTGTTGC 3660
NMB_MUT
AGCCTGGCACTGACTCTGGCCTCCTACCCATTCATTCAGCAAGCAAATAACGCCTGTTGC

NMB_REF ATGCCAGGCTTCGTGCC 3677

NMB_MUT ATGCCAGGCTTCGTGCC

Fig. 5 (cont:')

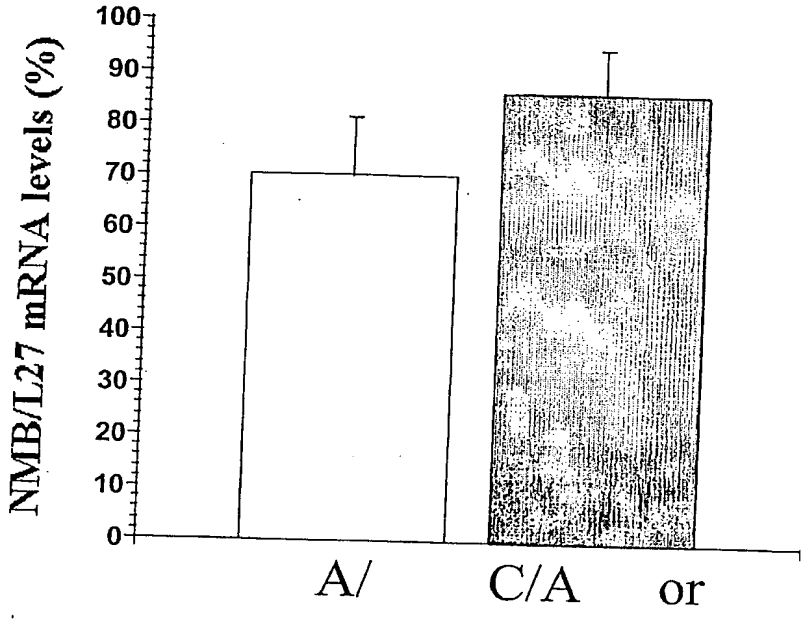

Fig. 6

g-433 C>T or rs1849288 (within NMB promoter)
NMB_REF
CTGTTACCCGGGAGGAGAGCTCCTCGCCCGACCTCTACCCTCATGAAGAGAGGCTCAGAG
NMB_MUT
CTGTTACCCGGGAGGAGAGCTCTTCGCCCGACCTCTACCCTCATGAAGAGAGGCTCAGAG

g.438 C>G or IVS1+281 C>G or rs2175567 (within NMB intron 1)
NMB_REF
TTACCTTAGGCGAGACTTAACCGAATCTTCTAACCGCTGGTGTGTTTTTGCTGCACCTCC
NMB_MUT
TTACCTTAGGCGAGACTTAACCGAATCTTCTAACGGCTGGTGTGTTTTTGCTGCACCTCC

g.630 C>A or IVS1+473 C>A or rs2292462 (within NMB intron 1)
NMB_REF
GGAAAAGCTGAGGGAGCAGGCTTTGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAG
NMB_MUT
GGAAAAGCTGAGGGAGCAGGATTTGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAG

g.864 C>A or c.217 C>A (position on the coding sequence (cDNA) from the NMB first codon) or p.P73T (within NMB exon 2) or rs1051168
NMB_REF
CCAGCCCATCCCCATTGGGGACAGCTCCCCACACCTCCCTGAGGGACCAGCGACTGCAGC
NMB_MUT
CCAGCCCATCCCCATTGGGGACAGCTACCCACACCTCCCTGAGGGACCAGCGACTGCAGC

g.1043 G>A or IVS2+66 G>A (unknown in databases) (within NMB intron 2)
NMB_REF
GGCCATCCCCGGATCCTGCATGGGAGGAATTACCACCCAGTACTGTATTAGGGTGTGACT
NMB_MUT
GGCCATCCCCGGATCCTGCATGGAAGGAATTACCACCCAGTACTGTATTAGGGTGTGACT

g.1173 G>C or IVS2+196 G>C(unknown in databases) (within NMB intron 2)
NMB_REF
GCAGAGCTCAAAGGAGGAACAGTCCAAAGAAAGGAAGCTGACCTTCCCAGTAGACCCCAT
NMB_MUT
GCAGAGCTCAAAGGAGGAACAGTCCAAACAAAGGAAGCTGACCTTCCCAGTAGACCCCAT

g.2493 A>G or IVS2-251 A>G or rs3809508 (within NMB intron 2)
NMB_REF
GTGAGGACGCTGACACTAGCCCAGCACCAAGCACTGTATTTGGATTTTCTTCCACGATCT
NMB_MUT
GTGAGGACGCTGACACTAGCCCAGCACCAGGCACTGTATTTGGATTTTCTTCCACGATCT

Fig. 7

g.2708 C>T or IVS2-36 C>T (unknown in databases) (within NMB intron 2)
NMB_REF
AATGGCAGGATGCCCCTATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTTCTGTATGT
NMB_MUT
AATGGCAGGATGCCCCTATCTTTATCAGGAGCCCTTCCCTGGCTCAATTCTTCTGTATGT

g.2817 T>C or g.*38 T>C or rs3748371 (within NMB 3' untranslated region)
NMB_REF
TAATGGGGCAGACACAACAGCGTGGCTTAGATTGTGCCCACCCAGGGAAGGTGCTGAATG
NMB_MUT
TAATGGGGCAGACACAACAGCGTGGCTTAGACTGTGCCCACCCAGGGAAGGTGCTGAATG

g.2863 C>G or g.*84 C>G or rs1804012 (within NMB 3' untranslated region)
NMB_REF
GTGCTGAATGGGACCCTGTTGATGGCCCCATCTGGATGTAAATCCTGAGCTCAAATCTCT
NMB_MUT
GTGCTGAATGGGACCCTGTTGATGGCCGCATCTGGATGTAAATCCTGAGCTCAAATCTCT

g.3022 C>A or g.*243 C>A or rs3748372 (within NMB 3' untranslated region)
NMB_REF
ATAAAACCTTGCTCTTTACATACAATGCCTGGTCCTCTCCTTTCACCCGTCTTTTAGGGG
NMB_MUT
ATAAAACCTTGCTCTTTACATAAAATGCCTGGTCCTCTCCTTTCACCCGTCTTTTAGGGG

Fig. 7 (cont')